IN THE SPECIFICATION:

Please amend the specification as follows:

Please amend the paragraph from page 2, line 21, through page 3, line 2, as follows:

Thus, measurements of biomarkers such as cartilage volume and cartilage thickness are made over the whole of the cartilage. However, measurements over the ~~w hole~~ whole of the cartilage ~~d o n ot p rovide c omplete i nformation c oncerning t he h ealth o f the c artilage~~ do not provide complete information concerning the health of the cartilage. ~~F or~~ For example, the inventors have discovered that in many conditions, the load-bearing regions of the cartilage, which are more stressed, have earlier and more advanced changes in biomarker measurements. The prior art provided no way to detect and assess those earlier and more advanced changes.

Please amend the paragraph on page 6, lines 14-18, as follows:

We selected five MR image sets from three healthy adult subjects who had participated ~~I n an in v ivo m agnetic resonance i maging o f a xial a nd a nterior l oads o f t heir~~ in an in vivo magnetic resonance imaging of axial and anterior loads of their knees. The MRI data sets were acquired with the subjects lying in a supine position in a loading device that was designed to comfortably position the knee joint with an average exion angle of 8°, depending on subject height.

Please amend the paragraph from page 7, line 21, through page 8, line 9, as follows:

Once the image sets were acquired, each one of them was analyzed using an automated method. The first step in the analysis consisted in the accurate extraction of the femur, tibia and patella subchondral bone plates from the Fast GRE MRI data sets. To achieve the desired accuracy we used a three stage supervised approach for the MRI segmentation. First, we use an unsupervised segmentation algorithm (Fig. 2, step 104) which has been used successfully to

3

segment bone structures from standard GRE sequences. Because ~~w e w ere d oing t he s egmentation o f f ast G RE s equences, t he a lgorithm d oes n ot~~ <u>we were doing the segmentations of fast GRE sequences, the algorithm does not</u> always make accurate estimations of the subchondral bone plates boundaries. Therefore, the second stage consisted of reviewing the segmentation, detecting the errors and correcting those using a tracing tool (Fig. 2, step 206). Once the user has decided that the segmentation of the femur and the tibia appear to be acceptable (Fig. 2, steps 208, 210), we arrive at the third stage: boundary relaxation (Fig. 2, step 212). The boundary relaxation uses a stochastic relaxation technique that uses the information from the segmentation and the MRI data sets to correct the boundary of the segmented structures.

Please amend the paragraph on page 10, lines 10-16, as follows:

The computation of biomarkers allows the identification of important structures or substructures, their normalities and abnormalities, and the identification of their specific topological, morphological, radiological, and pharmacokinetic characteristics which are sensitive indicators of joint disease and the state of pathology. The abnormality and normality ~~o f s tructures, along w ith t heir t opological a nd m orphological characteristics a nd~~ <u>of structures, along with their topological and morphological characteristics and</u> radiological and pharmacokinetic parameters, are used as the biomarkers, and specific measurements of the biomarkers serve as the quantitative assessment of joint disease.

4